



1/16

SEQUENCE LISTING

<110> Huang, Qian
Richmond, Joan F.L.
Cho, Bryan K.
Palliser, Deborah
Chen, Jianzhu
Eisen, Herman N.
Young, Richard A.

<120> In Vivo CTL Elicitation By Heat Shock
Protein Fusion Proteins Maps To A Discrete Domain and is
CD4+T Cell-Independent

<130> 0399.2006-003

<140> US 09/761,534

<141> 2001-01-16

<150> PCT/US00/32831

<151> 2000-12-01

<150> US 60/176,143

<151> 2000-01-14

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 tcg gtt ctg gaa ggt ggc gac ccg gtc gtc gtc gcc aac tcc gag ggc 96
 Ser Val Leu Glu Gly Gly Asp Pro Val Val Val Ala Asn Ser Glu Gly
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 tcc agg acc acc ccg tca att gtc gcg ttc gcc cgc aac ggt gag gtg 144
 Ser Arg Thr Thr Pro Ser Ile Val Ala Phe Ala Arg Asn Gly Glu Val
 35 40 45
 ctg gtc ggc cag ccc gcc aag aac cag gca gtg acc aac gtc gat cgc 192
 Leu Val Gly Gln Pro Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
 50 55 60

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Thr	Val	Arg	Ser	Val	Lys	Arg	His	Met	Gly	Ser	Asp	Trp	Ser	Ile	Glu	
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att	gac	ggc	aag	aaa	tac	acc	gcg	ccg	gag	atc	agc	gcc	cgc	att	ctg	288
Ile	Asp	Gly	Lys	Lys	Tyr	Thr	Ala	Pro	Glu	Ile	Ser	Ala	Arg	Ile	Leu	
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atg	aag	ctg	aag	cgc	gac	gcc	gag	gcc	tac	ctc	ggt	gag	gac	att	acc	336
Met	Lys	Leu	Lys	Arg	Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Ile	Thr	
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gac	gcg	gtt	atc	acg	acg	ccc	gcc	tac	ttc	aat	gac	gcc	cag	cgt	cag	384
Asp	Ala	Val	Ile	Thr	Thr	Pro	Ala	Tyr	Phe	Asn	Asp	Ala	Gln	Arg	Gln	
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gcc	acc	aag	gac	gcc	ggc	cag	atc	gcc	ggc	ctc	aac	gtg	ctg	cgg	atc	432
Ala	Thr	Lys	Asp	Ala	Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	
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gtc	aac	gag	ccg	acc	gcg	gcc	gcg	ctg	gcc	tac	ggc	ctc	gac	aag	ggc	480
Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Asp	Lys	Gly	
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Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Glu	Gly	Val	Val	Glu	Val	Arg	Ala	
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act	tcg	ggt	gac	aac	cac	ctc	ggc	ggc	gac	gac	tgg	gac	cag	cgg	gtc	624
Thr	Ser	Gly	Asp	Asn	His	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Val	
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Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Gln	
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Leu	Thr	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Asp	Arg	
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Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	
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Ala	Val	Thr	Asp	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Lys	Glu	Pro	Asn	
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Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln	
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gcc	ggc	gtc	ctc	aag	ggc	gag	gtg	aaa	gac	gtt	ctg	ctg	ctt	gat	gtt	1104
Ala	Gly	Val	Leu	Lys	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	
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acc	ccg	ctg	agc	ctg	ggg	atc	gag	acc	aag	ggc	ggg	gtg	atg	acc	agg	1152
Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Arg	
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ctc	atc	gag	cgc	aac	acc	acg	atc	ccc	acc	aag	cgg	tcg	gag	act	ttc	1200
Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe	
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Glu Lys Glu Gln Arg Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
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Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala
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Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu
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Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
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Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
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Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
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Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
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Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
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Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Arg
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Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
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Asp Val Ser Leu Leu Glu Ile Gly Glu Gly Val Val Glu Val Arg Ala	
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act tcg ggt gac aac cac ctc ggc ggc gac gac tgg gac cag cgg gtc	144
Thr Ser Gly Asp Asn His Leu Gly Gly Asp Asp Trp Asp Gln Arg Val	
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Val Asp Trp Leu Val Asp Lys Phe Lys Gly Thr Ser Gly Met Asp Leu	
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acc aag gac aag atg gcg atg cag cgg ctg cgg gaa gcc gcc gag aag	240
Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys	
65 70 75 80	
gca aag atc gag ctg agt tcg agt cag tcc acc tcg atc aac ctg ccc	288
Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro	
85 90 95	
tac atc acc gtc gac gcc gac aag aac ccg ttg ttc tta gac gag cag	336
Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln	
100 105 110	
ctg acc cgc gcg gag ttc caa cgg atc act cag gac ctg ctg gac cgc	384
Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg	
115 120 125	
act cgc aag ccg ttc cag tcg gtg atc gct gac acc ggc att tcg gtg	432
Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val	
130 135 140	
tcg gag atc gat cac gtt gtg ctc gtg ggt ggt tcg acc cgg atg ccc	480
Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro	
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Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn	
165 170 175	
aag ggc gtc aac ccc gat gag gtt gtc gcg gtg gga gcc gct ctg cag	576
Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln	
180 185 190	
gcc ggc gtc ctc aag ggc gag gtg aaa gac gtt ctg ctg ctt gat gtt	624
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 35 40 45
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 50 55 60
 Thr Lys Asp Lys Met Ala Met Gln Arg Leu Arg Glu Ala Ala Glu Lys
 65 70 75 80
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Thr Ser Ile Asn Leu Pro
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 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Gln
 100 105 110
 Leu Thr Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Asp Arg
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 Thr Arg Lys Pro Phe Gln Ser Val Ile Ala Asp Thr Gly Ile Ser Val
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 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
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 Ala Val Thr Asp Leu Val Lys Glu Leu Thr Gly Gly Lys Glu Pro Asn
 165 170 175
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Gln	Gly	Asn	Arg	Thr	Thr	Pro	Ser	Tyr	Val	Ala	Phe	Thr	Asp	Thr	Glu	
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Asn	Thr	Val	Phe	Asp	Ala	Lys	Arg	Leu	Ile	Gly	Arg	Lys	Phe	Gly	Asp	
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Ser	Glu	Asn	Val	Gln	Asp	Leu	Leu	Leu	Leu	Asp	Val	Ala	Pro	Leu	Ser	
385					390					395					400	
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Leu	Gly	Leu	Glu	Thr	Ala	Gly	Gly	Val	Met	Thr	Ala	Leu	Ile	Lys	Arg	
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aac	tcc	acc	atc	ccc	acc	aag	cag	acg	cag	acc	ttc	acc	acc	tac	tcg	1296
Asn	Ser	Thr	Ile	Pro	Thr	Lys	Gln	Thr	Gln	Thr	Phe	Thr	Thr	Tyr	Ser	
			420					425					430			
gac	aac	cag	ccc	ggg	gtg	ctg	atc	cag	gtg	tac	gag	ggc	gag	agg	gcc	1344
Asp	Asn	Gln	Pro	Gly	Val	Leu	Ile	Gln	Val	Tyr	Glu	Gly	Glu	Arg	Ala	
		435					440					445				
atg	acg	cgc	gac	aac	aac	ctg	ctg	ggg	cgc	ttc	gag	ctg	agc	ggc	atc	1392
Met	Thr	Arg	Asp	Asn	Asn	Leu	Leu	Gly	Arg	Phe	Glu	Leu	Ser	Gly	Ile	
	450					455					460					
ccg	ccg	gcg	ccc	agg	ggc	gtg	ccg	cag	atc	gag	gtg	acc	ttc	gac	atc	1440
Pro	Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile	
465					470					475					480	

gac gcc aac ggc atc ctg aac gtc acg gcc acc gac aag agc acc ggc	1488
Asp Ala Asn Gly Ile Leu Asn Val Thr Ala Thr Asp Lys Ser Thr Gly	
485 490 495	
aag gcc aac aag atc acc atc acc aac gac aag ggc cgc ctg agc aag	1536
Lys Ala Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys	
500 505 510	
gag gag atc gag cgc atg gtg cag gag gcc gag cgc tac aag gcc gag	1584
Glu Glu Ile Glu Arg Met Val Gln Glu Ala Glu Arg Tyr Lys Ala Glu	
515 520 525	
gac gag gtg cag cgc gac agg gtg gcc gcc aag aac gcg ctc gag tcc	1632
Asp Glu Val Gln Arg Asp Arg Val Ala Ala Lys Asn Ala Leu Glu Ser	
530 535 540	
tat gcc ttc aac atg aag agc gcc gtg gag gac gag ggt ctc aag ggc	1680
Tyr Ala Phe Asn Met Lys Ser Ala Val Glu Asp Glu Gly Leu Lys Gly	
545 550 555 560	
aag ctc agc gag gct gac aag aag aag gtc ctg gac aag tgc cag gag	1728
Lys Leu Ser Glu Ala Asp Lys Lys Lys Val Leu Asp Lys Cys Gln Glu	
565 570 575	
gtc atc tcc tgg ctg gac tcc aac acg ctg gcc gac aag gag gag ttc	1776
Val Ile Ser Trp Leu Asp Ser Asn Thr Leu Ala Asp Lys Glu Glu Phe	
580 585 590	
gtg cac aag cgg gag gag ctg gag cgg gtg tgc agc ccc atc atc agt	1824
Val His Lys Arg Glu Glu Leu Glu Arg Val Cys Ser Pro Ile Ile Ser	
595 600 605	
ggg ctg tac cag ggt gcg ggt gct cct ggg gct ggg ggc ttc ggg gcc	1872
Gly Leu Tyr Gln Gly Ala Gly Ala Pro Gly Ala Gly Gly Phe Gly Ala	
610 615 620	
cag gcg ccg ccg aaa gga gcc tct ggc tca gga ccc acc atc gag gag	1920
Gln Ala Pro Pro Lys Gly Ala Ser Gly Ser Gly Pro Thr Ile Glu Glu	
625 630 635 640	
gtg gat tag	1929
Val Asp *	

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 Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile Ile Ala Asn Asp
 20 25 30

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		35					40					45			
Arg	Leu	Ile	Gly	Asp	Ala	Ala	Lys	Asn	Gln	Val	Ala	Leu	Asn	Pro	Gln
	50				55						60				
Asn	Thr	Val	Phe	Asp	Ala	Lys	Arg	Leu	Ile	Gly	Arg	Lys	Phe	Gly	Asp
65					70					75					80
Ala	Val	Val	Gln	Ser	Asp	Met	Lys	His	Trp	Pro	Phe	Gln	Val	Val	Asn
				85					90					95	
Asp	Gly	Asp	Lys	Pro	Lys	Val	Gln	Val	Asn	Tyr	Lys	Gly	Glu	Ser	Arg
			100						105				110		
Ser	Phe	Phe	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Thr	Lys	Met	Lys
	115						120					125			
Glu	Ile	Ala	Glu	Ala	Tyr	Leu	Gly	His	Pro	Val	Thr	Asn	Ala	Val	Ile
	130					135					140				
Thr	Val	Pro	Ala	Tyr	Phe	Asn	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Asp
145					150					155					160
Ala	Gly	Val	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Ile	Asn	Glu	Pro
				165					170					175	
Thr	Ala	Ala	Ala	Ile	Ala	Tyr	Gly	Leu	Asp	Arg	Thr	Gly	Lys	Gly	Glu
			180				185						190		
Arg	Asn	Val	Leu	Ile	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser
	195						200					205			
Ile	Leu	Thr	Ile	Asp	Asp	Gly	Ile	Phe	Glu	Val	Lys	Ala	Thr	Ala	Gly
	210					215					220				
Asp	Thr	His	Leu	Gly	Gly	Glu	Asp	Phe	Asp	Asn	Arg	Leu	Val	Ser	His
225					230					235					240
Phe	Val	Glu	Glu	Phe	Lys	Arg	Lys	His	Lys	Lys	Asp	Ile	Ser	Gln	Asn
				245					250					255	
Lys	Arg	Ala	Val	Arg	Arg	Leu	Arg	Thr	Ala	Cys	Glu	Arg	Ala	Lys	Arg
			260					265					270		
Thr	Leu	Ser	Ser	Ser	Thr	Gln	Ala	Ser	Leu	Glu	Ile	Asp	Ser	Leu	Phe
	275					280						285			
Glu	Gly	Ile	Asp	Phe	Tyr	Thr	Ser	Ile	Thr	Arg	Ala	Arg	Phe	Glu	Glu
	290					295					300				
Leu	Cys	Ser	Asp	Leu	Phe	Arg	Gly	Thr	Leu	Glu	Pro	Val	Glu	Lys	Ala
305					310					315					320
Leu	Arg	Asp	Ala	Lys	Met	Asp	Lys	Ala	Gln	Ile	His	Asp	Leu	Val	Leu
				325					330					335	
Val	Gly	Gly	Ser	Thr	Arg	Ile	Pro	Lys	Val	Gln	Lys	Leu	Leu	Gln	Asp
			340					345					350		
Phe	Phe	Asn	Gly	Arg	Asp	Leu	Asn	Lys	Ser	Ile	Asn	Pro	Asp	Glu	Ala
		355					360					365			
Val	Ala	Tyr	Gly	Ala	Ala	Val	Gln	Ala	Ala	Ile	Leu	Met	Gly	Asp	Lys
	370					375					380				
Ser	Glu	Asn	Val	Gln	Asp	Leu	Leu	Leu	Leu	Asp	Val	Ala	Pro	Leu	Ser
385					390					395					400
Leu	Gly	Leu	Glu	Thr	Ala	Gly	Gly	Val	Met	Thr	Ala	Leu	Ile	Lys	Arg
				405					410					415	
Asn	Ser	Thr	Ile	Pro	Thr	Lys	Gln	Thr	Gln	Thr	Phe	Thr	Thr	Tyr	Ser
			420					425					430		
Asp	Asn	Gln	Pro	Gly	Val	Leu	Ile	Gln	Val	Tyr	Glu	Gly	Glu	Arg	Ala
							440					445			
Met	Thr	Arg	Asp	Asn	Asn	Leu	Leu	Gly	Arg	Phe	Glu	Leu	Ser	Gly	Ile
	450					455					460				
Pro	Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile
465					470					475					480
Asp	Ala	Asn	Gly	Ile	Leu	Asn	Val	Thr	Ala	Thr	Asp	Lys	Ser	Thr	Gly
				485					490					495	
Lys	Ala	Asn	Lys	Ile	Thr	Ile	Thr	Asn	Asp	Lys	Gly	Arg	Leu	Ser	Lys

			500					505					510			
Glu	Glu	Ile	Glu	Arg	Met	Val	Gln	Glu	Ala	Glu	Arg	Tyr	Lys	Ala	Glu	
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Asp	Glu	Val	Gln	Arg	Asp	Arg	Val	Ala	Ala	Lys	Asn	Ala	Leu	Glu	Ser	
	530					535					540					
Tyr	Ala	Phe	Asn	Met	Lys	Ser	Ala	Val	Glu	Asp	Glu	Gly	Leu	Lys	Gly	
545					550					555					560	
Lys	Leu	Ser	Glu	Ala	Asp	Lys	Lys	Lys	Val	Leu	Asp	Lys	Cys	Gln	Glu	
			565					570						575		
Val	Ile	Ser	Trp	Leu	Asp	Ser	Asn	Thr	Leu	Ala	Asp	Lys	Glu	Glu	Phe	
		580					585					590				
Val	His	Lys	Arg	Glu	Glu	Leu	Glu	Arg	Val	Cys	Ser	Pro	Ile	Ile	Ser	
	595					600					605					
Gly	Leu	Tyr	Gln	Gly	Ala	Gly	Ala	Pro	Gly	Ala	Gly	Gly	Phe	Gly	Ala	
	610					615				620						
Gln	Ala	Pro	Pro	Lys	Gly	Ala	Ser	Gly	Ser	Gly	Pro	Thr	Ile	Glu	Glu	
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Val	Asp															

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 <213> Unknown

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 <223> Murine hsp70 -Segment II

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Lys	Gly	Glu	Arg	Asn	Val	Leu	Ile	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe		
1				5					10					15			
gac	gtg	tcc	atc	ctg	acg	atc	gac	gac	ggc	atc	ttc	gag	gtg	aag	gcc	96	
Asp	Val	Ser	Ile	Leu	Thr	Ile	Asp	Asp	Gly	Ile	Phe	Glu	Val	Lys	Ala		
			20				25						30				
acg	gcg	ggc	gac	acg	cac	ctg	gga	ggg	gag	gac	ttc	gac	aac	cgg	ctg	144	
Thr	Ala	Gly	Asp	Thr	His	Leu	Gly	Gly	Glu	Asp	Phe	Asp	Asn	Arg	Leu		
		35				40					45						
gtg	agc	cac	ttc	gtg	gag	gag	ttc	aag	agg	aag	cac	aag	aag	gac	atc	192	
Val	Ser	His	Phe	Val	Glu	Glu	Phe	Lys	Arg	Lys	His	Lys	Lys	Asp	Ile		
	50					55					60						
agc	cag	aac	aag	cgc	gcg	gtg	cgg	cgg	ctg	cgc	acg	gcg	tgt	gag	agg	240	
Ser	Gln	Asn	Lys	Arg	Ala	Val	Arg	Arg	Leu	Arg	Thr	Ala	Cys	Glu	Arg		
65					70				75					80			
gcc	aag	agg	acg	ctg	tcg	tcc	agc	acc	cag	gcc	agc	ctg	gag	atc	gac	288	
Ala	Lys	Arg	Thr	Leu	Ser	Ser	Ser	Thr	Gln	Ala	Ser	Leu	Glu	Ile	Asp		
				85					90					95			

tct ctg ttc gag ggc atc gac ttc tac aca tcc atc acg cgg gcg cgg	336
Ser Leu Phe Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg	
100 105 110	
ttc gaa gag ctg tgc tgc gac ctg ttc cgc ggc acg ctg gag ccc gtg	384
Phe Glu Glu Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val	
115 120 125	
gag aag gcc ctg cgc gac gcc aag atg gac aag gcc cag atc cac gac	432
Glu Lys Ala Leu Arg Asp Ala Lys Met Asp Lys Ala Gln Ile His Asp	
130 135 140	
ctg gtg ctg gtg ggc ggc tgc acg cgc atc ccc aag gtg cag aag ctg	480
Leu Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys Val Gln Lys Leu	
145 150 155 160	
ctg cag gac ttc ttc aac ggg cgc gac ctg aac aag agc atc aac ccg	528
Leu Gln Asp Phe Phe Asn Gly Arg Asp Leu Asn Lys Ser Ile Asn Pro	
165 170 175	
gac gag gcg gtg gcc tac ggg gcg gcg gtg cag gcg gcc atc ctg atg	576
Asp Glu Ala Val Ala Tyr Gly Ala Val Gln Ala Ala Ile Leu Met	
180 185 190	
ggg gac aag tgc gag aac gtg cag gac ctg ctg ctg ctg gac gtg gcg	624
Gly Asp Lys Ser Glu Asn Val Gln Asp Leu Leu Leu Leu Asp Val Ala	
195 200 205	
ccc	627
Pro	

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 <211> 209
 <212> PRT
 <213> Unknown

<220>
 <223> Murine hsp70 - Segment II

<400> 12

Lys Gly Glu Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe	
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Asp Val Ser Ile Leu Thr Ile Asp Asp Gly Ile Phe Glu Val Lys Ala	
20 25 30	
Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Leu	
35 40 45	
Val Ser His Phe Val Glu Glu Phe Lys Arg Lys His Lys Lys Asp Ile	
50 55 60	
Ser Gln Asn Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg	
65 70 75 80	
Ala Lys Arg Thr Leu Ser Ser Ser Thr Gln Ala Ser Leu Glu Ile Asp	
85 90 95	
Ser Leu Phe Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg	
100 105 110	
Phe Glu Glu Leu Cys Ser Asp Leu Phe Arg Gly Thr Leu Glu Pro Val	
115 120 125	

Glu	Lys	Ala	Leu	Arg	Asp	Ala	Lys	Met	Asp	Lys	Ala	Gln	Ile	His	Asp
	130					135					140				
Leu	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Ile	Pro	Lys	Val	Gln	Lys	Leu
145					150					155					160
Leu	Gln	Asp	Phe	Phe	Asn	Gly	Arg	Asp	Leu	Asn	Lys	Ser	Ile	Asn	Pro
			165						170					175	
Asp	Glu	Ala	Val	Ala	Tyr	Gly	Ala	Ala	Val	Gln	Ala	Ala	Ile	Leu	Met
			180					185					190		
Gly	Asp	Lys	Ser	Glu	Asn	Val	Gln	Asp	Leu	Leu	Leu	Leu	Asp	Val	Ala
		195					200						205		
Pro															

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 <213> Unknown

<220>
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<400> 13
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<210> 14
 <211> 63
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 <213> Unknown

<220>
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 agt 63

<210> 15
 <211> 44
 <212> DNA
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<220>
 <223> PCR Primer oQH001

<400> 15
 atagtactgg atccatggct cgtgcggtcg ggatcgacct cggg 44

<210> 16
 <211> 36
 <212> DNA
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<400> 16
 ggaattccta tctagtcact tgcctccccg gccgtc 36

<210> 17
<211> 49
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<220>
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gtcgcacgaat tcacatcacag attcgctgct ccttctcgcc cttgtcgag 49

<210> 18
<211> 48
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<220>
<223> PCR Primer oQH012

<400> 18
gtcgcacggat ccatggagaa ggagcagcga atcctggctc tcgacttg 48

<210> 19
<211> 48
<212> DNA
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<220>
<223> PCR Primer oQH014

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gtcgcacggat ccatgggtgaa agacgttctg ctgcttgatg ttaccccg 48

<210> 20
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<212> DNA
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gtcgcacggat ccatgcgtaa tcaagccgag acattggctc accagacg 48

<210> 21
<211> 49
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<210> 22
 <211> 49
 <212> DNA
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<220>
 <223> PCR Primer oQH015

<400> 22
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<210> 23
 <211> 33
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<220>
 <223> PCR Primer oJR12

<400> 23
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<210> 24
 <211> 39
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 <213> Unknown

<220>
 <223> PCR Primer oJR103

<400> 24
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<210> 25
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 <212> PRT
 <213> Unknown

<220>
 <223> P1 Peptide

<400> 25
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 Gly Leu Leu Leu Lys Glu Ala Tyr
 20